

In the specification:

Please amend the specification as follows:

Please delete the paragraph on page 2, lines 16-22 and replace it with the following paragraph:

Figure 1 depicts an alignment of the amino acid sequences of the PRSS11-L protein (SEQ ID NO: 2) and the two other S2 serine proteases, PRSS11 (SEQ ID NO: 9) (Genbank Protein ID: CAA69226) and Omi (SEQ ID NO: 10) (Genbank Protein ID: AAB94569). The alignment was performed using the Wisconsin GCG Gap Needleman and Wunsch algorithm. The active site residues of the catalytic triad are indicated above the sequences by asterisks (*).

Please delete the paragraph on page 2, lines 23-26 and replace it with the following paragraph:

Figure 2 depicts an alignment of the amino acid sequences of the PRSS11-L protein (SEQ ID NO: 2) and HtrA3 (SEQ ID NO: 11) (Genbank Protein ID: AAH34390). The alignment was performed using the Wisconsin GCG Gap Needleman and Wunsch algorithm.

Please delete the paragraph on page 3, lines 5-7 and replace it with the following paragraph:

Figure 4 shows the splice donor/acceptor sites for human HtrA3 and PRSS11-L transcripts on the HtrA3 gene. E stands for exon. Figure discloses SEQ ID NOS: 12-29, respectively, in order of appearance.

Please delete the paragraph on page 13, lines 11-27, and replace it with the following paragraph:

A preferred, non-limiting example of a mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin et al., (1990), Proc. Natl. Acad. Sci. USA 87:2264-2268, modified as in Karlin et al., (1993), Proc. Natl. Acad. Sci. USA 90:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul et al., (1990), J. Mol. Biol 215:403-410. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in

Altschul et al., (1997), Nucleic Acids Res. 25:3389-3402. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>. Additionally, there is the FASTA method (Atschul et al., (1990), J. Molec. Biol. 215, 403), which can be used.

Please delete the paragraph on page 79, lines 3-25 and replace it with the following paragraph:

Sequence alignment revealed that PRSS11-L protein shared strong homology to the catalytic domains of the other two human S2 serine proteases (Fig. 1). Motifs shared by all three human S2 serine proteases are TNAHVV (SEQ ID NO: 30), DIA and GNSGGPLVNLDGEVIG (SEQ ID NO: 31) within the catalytic domains with the catalytic triad residues H, D and S of protease PRSS11-L located at positions 72, 108 and 186, respectively (using the methionine initiator of the PRSS11-L sequence as number one) (Fig. 1). In addition, the catalytic domains of these three S2 proteases appears to be flanked by an SH3 domain at the amino terminus and a PDZ domain at the C-terminus, both domains are importantly involved protein-interaction (Mayer, (2000), *J. Cell Science* 114: 1253-1263; Sheng et al., (2001), *Annu. Rev. Neurosci.* 24:1-29). Therefore, PRSS11-L can interact with other proteins through these interactions interfaces. It is formally possible that the PRSS11-L protein is initially synthesized as an inactive zymogen precursor, which requires one or more limited proteolytic cleavages to become active. Because PRSS11-L protein appears to lack any hydrophobic amino acid stretch consistent with either a signal sequence or transmembrane domain, it is not likely to be secreted or an integral membrane protein.